

FIG. 1

Escherichia coli
Escherichia coli

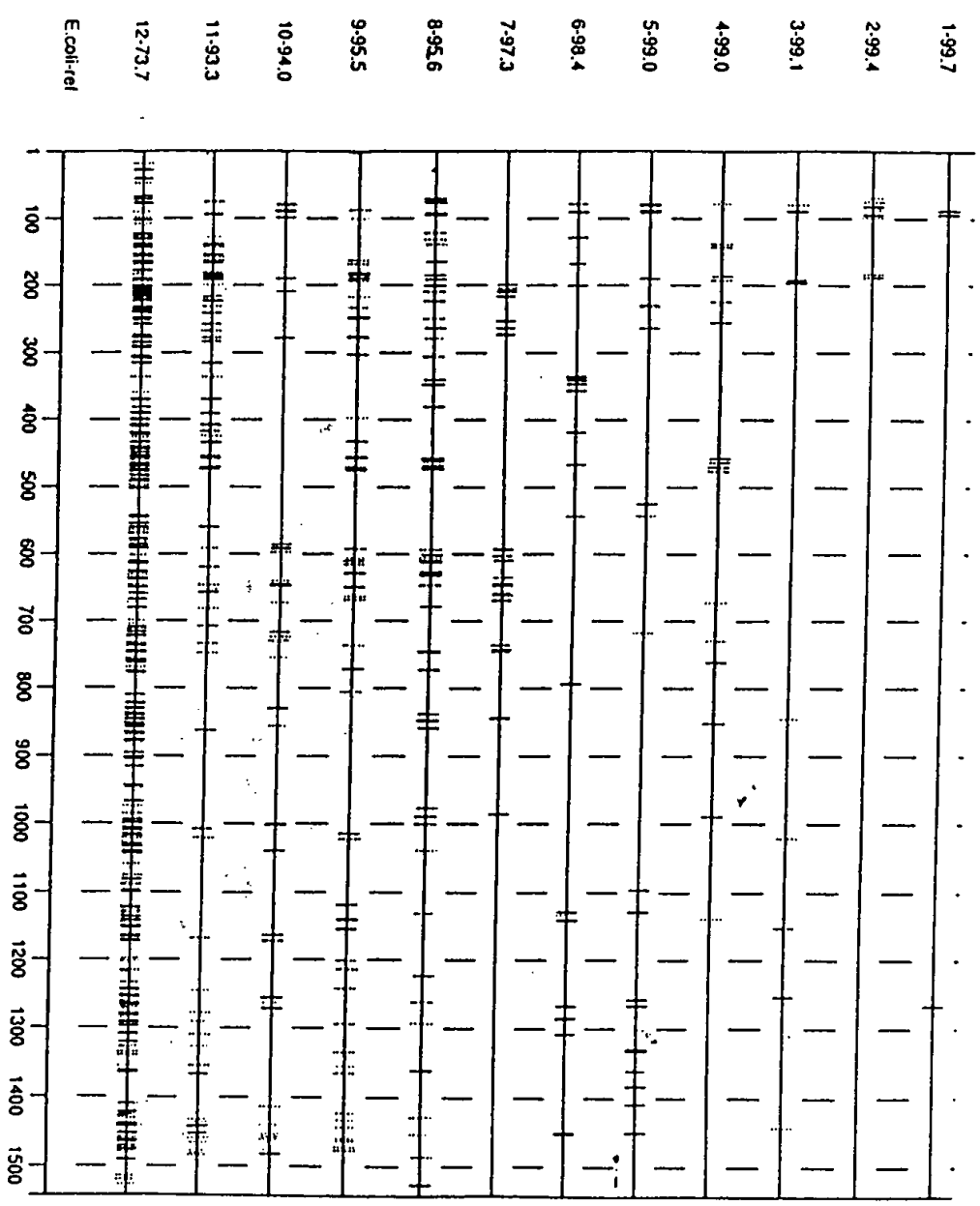
UCCUUGCCGCCGUAACCGCGUGUCCGACCUCAACCCCAUCCGCAACUACAAGUGAAACCGUAACCGCAUCCUAGUGUGGCGUUCGCCCAUCCGAC
AGUACCAACUCCGACCAU

100
120

FIG. 3

[illegible]

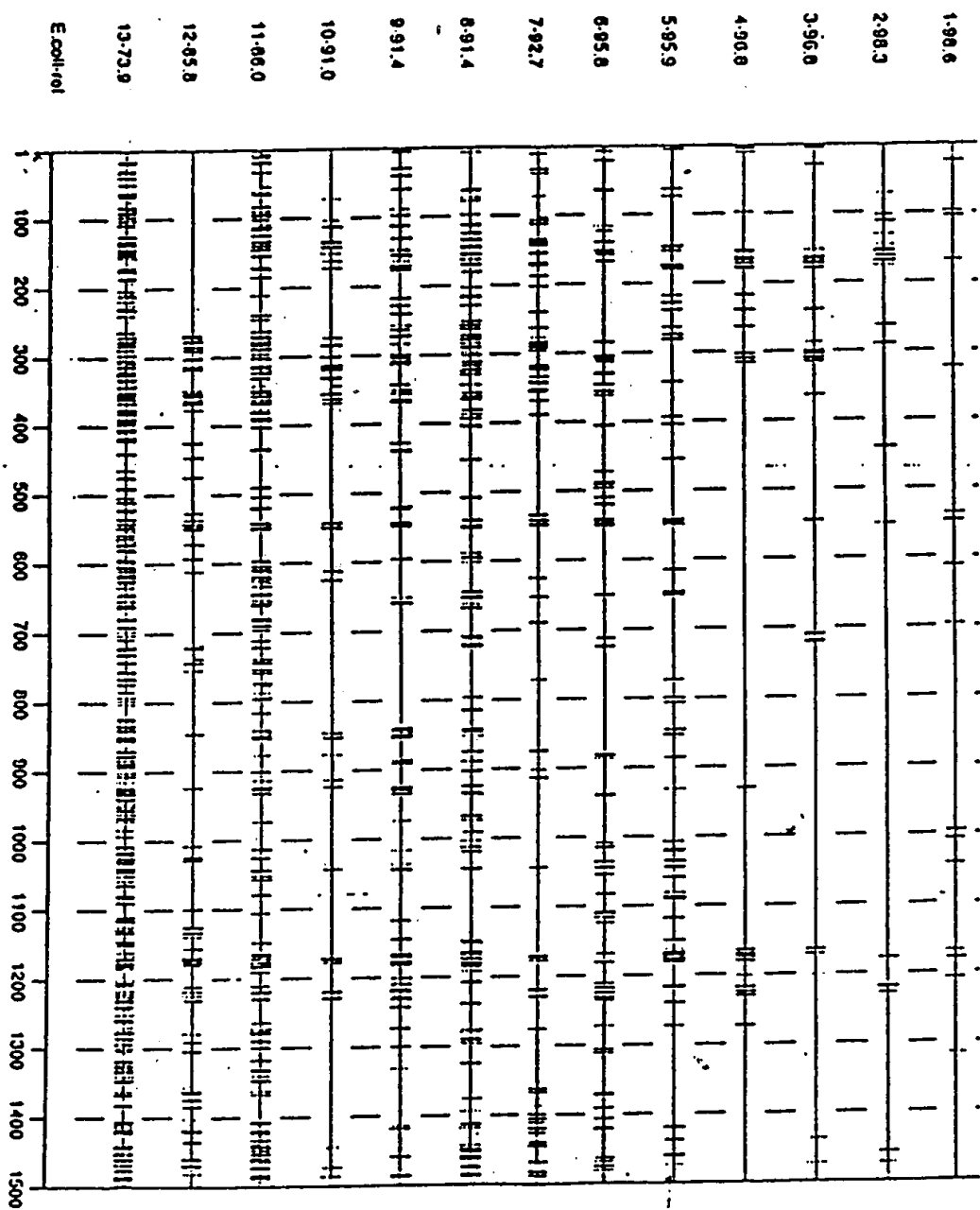
FIG. 6
Summary of 16S rRNA Analysis



LEGEND: Summary of 16S rRNA Analysis (Listing of Bacteria and percent similarity included in analysis)

1. 99.7% Clostridium botulinum G-Clostridium subterminale; 2. 99.4% Streptococcus cremoris-Streptococcus lactis; 3. 99.1% Lactobacillus lactis-Lactobacillus delbrueckii;
4. 99.0% Neisseria gonorrhoeae-Neisseria meningitidis; 5. 99.0% Mycobacterium intracellulare Mycobacterium avium; 6. 98.4% Mycobacterium avium-Mycobacterium tuberculosis; 7. 97.3% Pseudomonas alcaligenes-Pseudomonas stutzeri; 8. 95.6% Chlamydia psittaci-Chlamydia trachomatis;
9. 95.5% Spiroplasma citri-Spiroplasma mirum; 10. 94.0% Clostridium lituseburense-Clostridium sodellii; 11. 93.3% Listeria monocytogenes-Brochothrix thermosphacta; 12. 73.7% Escherichia coli-Bacteroides fragilis.

FIG. 7
Summary of 23S rRNA Analysis

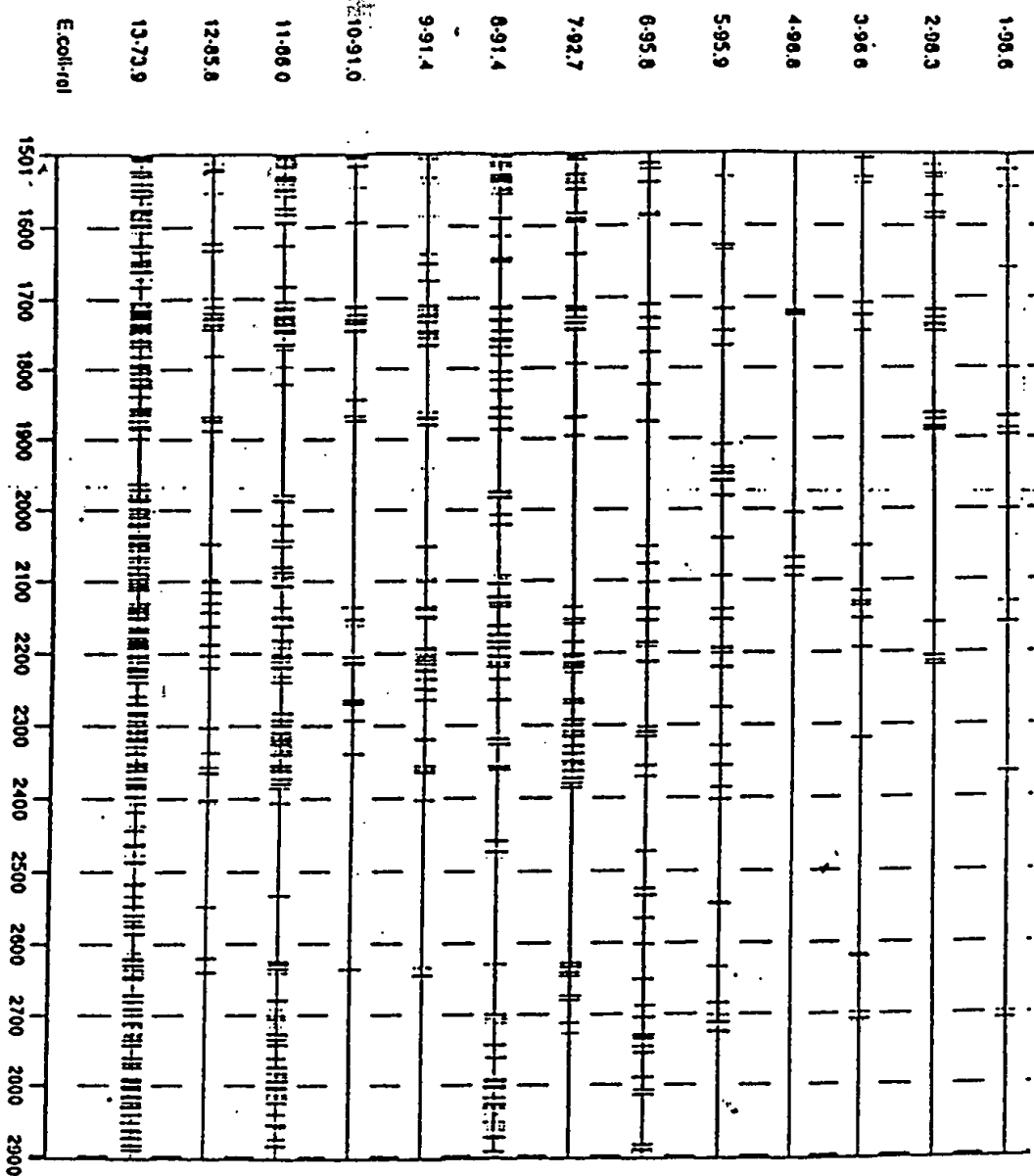


LEGEND: Summary of 23S rRNA Analysis (Listing of Bacteria and percent similarity included in analysis)

1. 98.6% *Neisseria gonorrhoeae*-*Neisseria meningitidis*; 2. 98.3% *Proteus mirabilis*-*Proteus vulgaris*; 3. 96.8% *Mycobacterium intracellulare*-*Mycobacterium avium*; 4. 96.8% *Mycobacterium avium*-*Mycobacterium asiaticum*; 5. 95.9% *Mycobacterium tuberculosis*-*Mycobacterium kansasii*; 6. 95.8% *Nicotiana tabacum* (tobacco)-*Zea mays* (maize); 7. 92.7% *Proteus vulgaris*-*Klebsiella rhinoscleromatis*; 8. 91.4% *Bacillus stearothermophilus*-*Bacillus subtilis*; 9. 91.4% *Mycobacterium intracellulare*-*Mycobacterium fortuitum*; 10. 91.0% *Escherichia coli*-*Klebsiella rhinoscleromatis*; 11. 86.0% *Escherichia coli*-*Pseudomonas aeruginosa*; 12. 85.8% *Chlamydia trachomatis*-*Chlamydia psittaci*; 13. 73.9% *Escherichia coli*-*Anacystis nidulans*.

FIG. 8

Summary of 23S rRNA Analysis



LEGEND: Summary of 23S rRNA Analysis (Listing of Bacteria and percent similarity included in analysis)

1. 98.6% *Neisseria gonorrhoeae*-*Neisseria meningitidis*; 2. 98.3% *Proteus mirabilis*-*Proteus vulgaris*; 3. 96.8% *Mycobacterium intracellulare*-*Mycobacterium avium*; 4. 96.8% *Mycobacterium avium*-*Mycobacterium asiaticum*; 5. 95.9% *Mycobacterium tuberculosis*-*Mycobacterium kansasii*; 6. 95.8% *Nicotiana tabacum* (tobacco)-*Zea mays* (maize); 7. 92.7% *Proteus vulgaris*-*Klebsiella rhinoscleromatis*; 8. 91.4% *Bacillus stearothermophilus*-*Bacillus subtilis*; 9. 91.4% *Mycobacterium intracellulare*-*Mycobacterium fortuitum*; 10. 91.0% *Escherichia coli*-*Klebsiella rhinoscleromatis*; 11. 86.0% *Escherichia coli*-*Pseudomonas aeruginosa*; 12. 85.8% *Chlamydia trachomatis*-*Chlamydia psittaci*; 13. 73.9% *Escherichia coli*-*Anacystis nidulans*.

Summary of 16S rRNA PROBE locations

00/454529

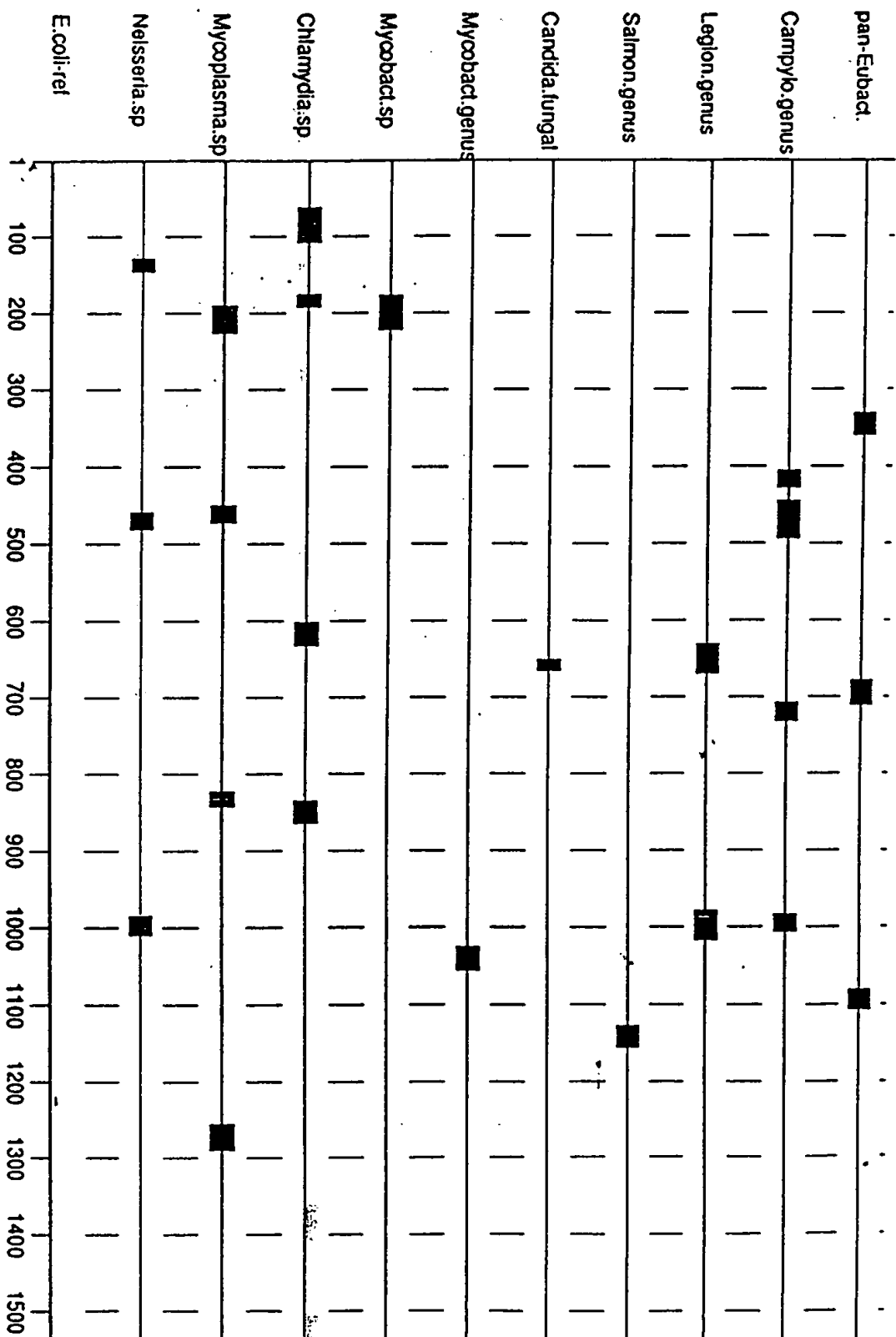


FIG. 9

Summary of 23S rRNA PROBE locations

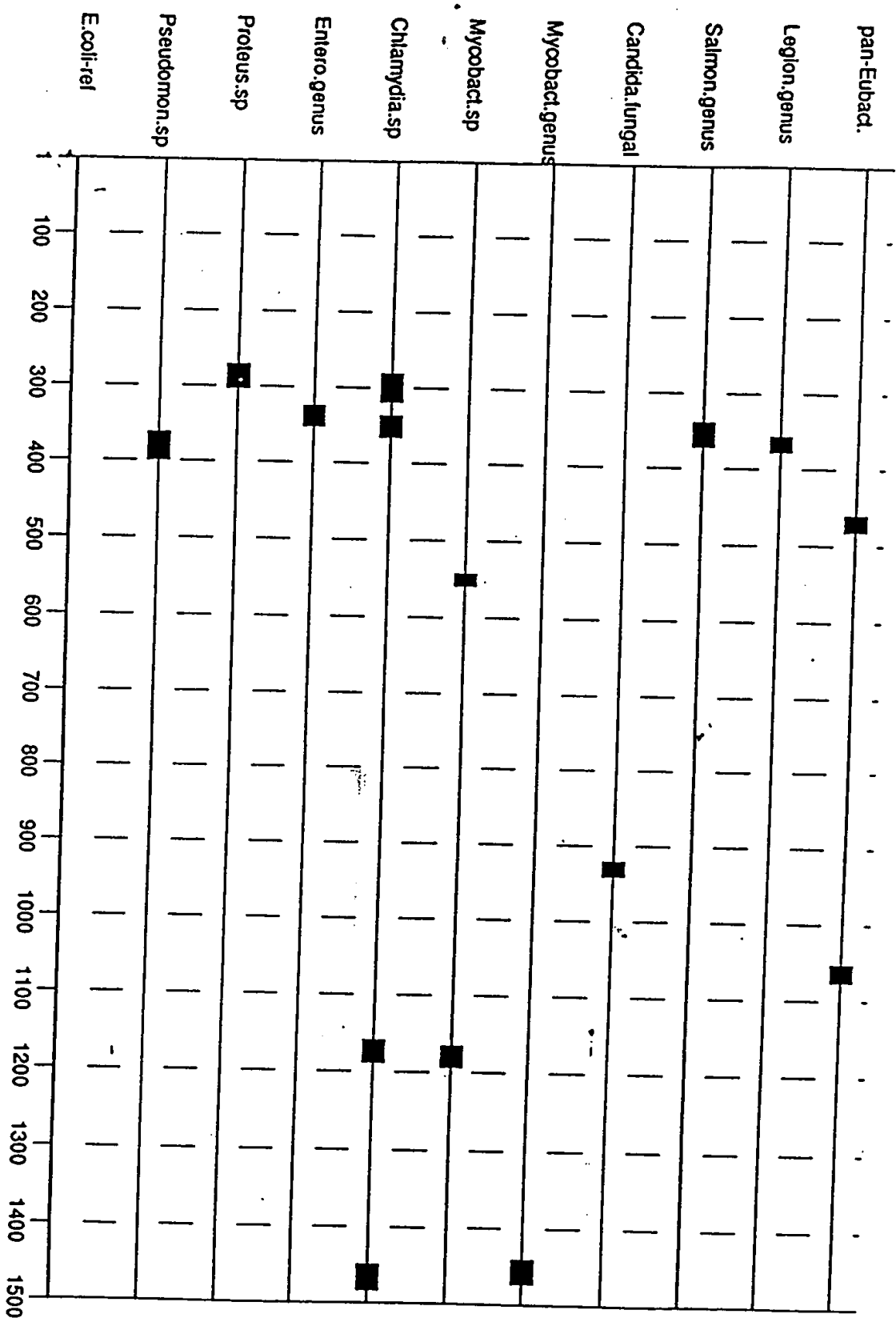


FIG. 10

Summary of 23S rRNA PROBE locations

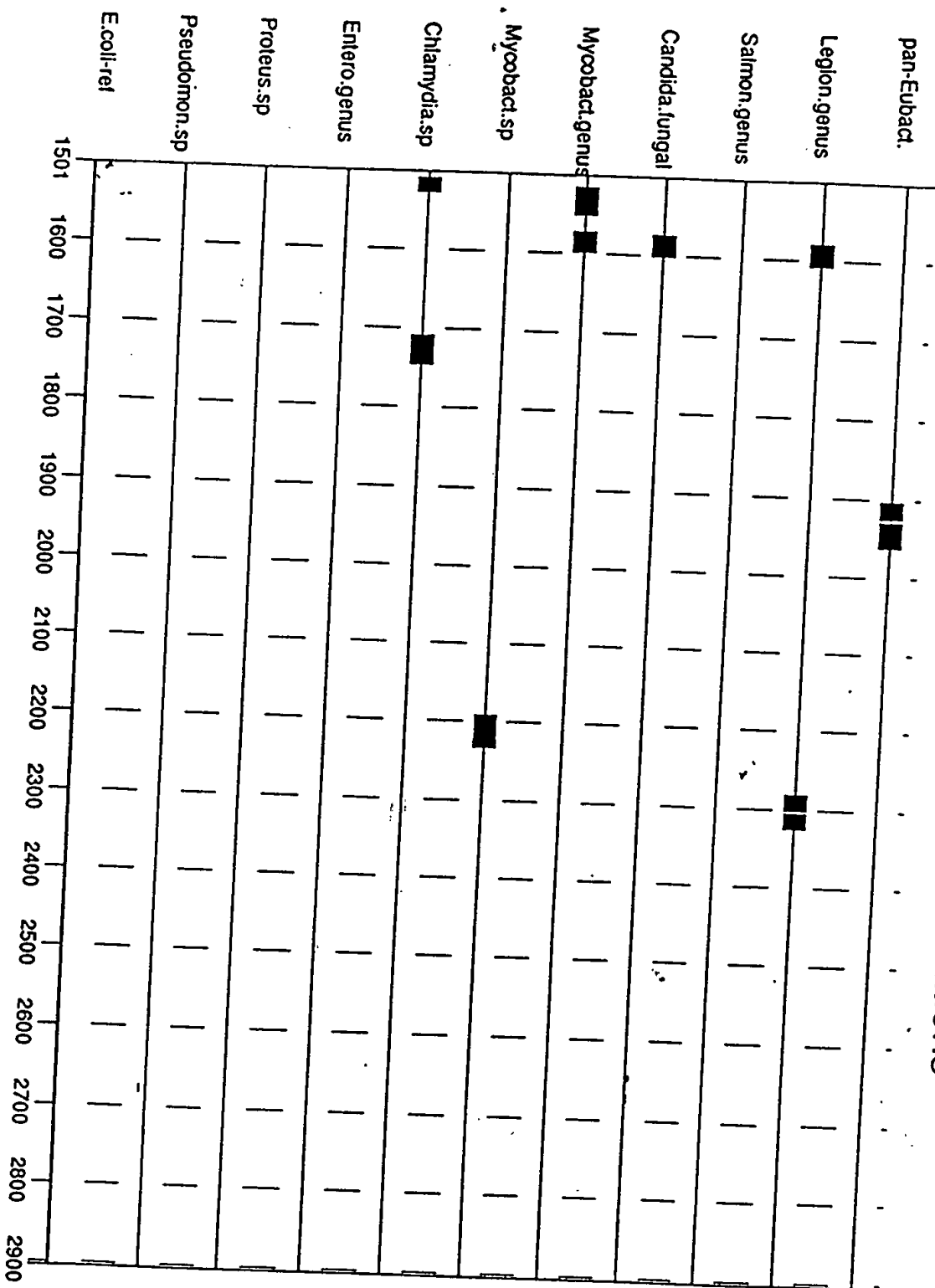


FIG. 11